

SEQUENCE LISTING

<110> Tang, Y. Tom
 Liu, Chenghua
 Zhou, Ping
 Asundi, Vinod
 Zhang, Jie
 Zhao, Qing A.
 Ren, Feiyan
 Xue, Aidong J.
 Yang, Yonghong
 Wehrman, Tom
 Drmanac, Radoje T.

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 Polypeptides

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Ser Ala Ser Thr Phe Ser Pro Asp Gly Arg Val Phe Gln Val Glu Tyr
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Gln Asn Gly Pro Met Asn Gly Cys Glu Lys Asp Ser Ser Ser Thr Asp						
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360 365 370 375	

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Ala	His	Ala	Ala	Thr 380	Ser	Gly	Lys	Gln 385	Ser	Asn	Phe	Ser	Arg	Lys Ser 390		
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Ser	Thr	His	Asn 395	Lys	Pro	Ser	Glu	Gly 400	Lys	Ala	Ala	Asn	Pro	Lys Met 405		
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Val	Ser	Ser	Leu 410	Pro	Ser	Thr	Ala	Asp 415	Pro	Ser	His	Gln	Thr	Met Pro 420		
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Ala	Asn	Lys	Gln	Asn	Gly	Ser	Ser	Asn	Gln	Arg	Arg	Arg	Phe	Asn Pro 435		
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Gln	Tyr	His	Asn	Asn	Arg	Leu	Asn	Gly	Pro	Ala	Lys	Ser	Gln	Gly Ser 455		
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Gly	Asn	Glu	Ala	Glu	Pro	Leu	Gly	Lys	Gly	Asn	Ser	Arg	His	Glu His 470		
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Arg	Arg	Gln	Pro	His	Asn	Gly	Phe	Arg	Pro	Lys	Asn	Lys	Gly	Gly Ala 485		
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Lys	Asn	Gln	Glu	Ala	Ser	Leu	Gly	Met	Lys	Thr	Pro	Glu	Ala	Pro Ala 500		
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His	Ser	Glu	Lys	Pro	Arg	Arg	Arg	Gln	His	Ala	Ala	Asp	Thr	Ser Glu 515		
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Cys	Pro	Thr	Arg	Ile	Glu	Val	Ser	Thr	Asp	Ala	Ala	Val	Leu	Ser Val 550		
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Pro	Ala	Val	Thr	Leu	Val	Ala	*									
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gtaacttgg	tattacacac	acgtttggag	cccagtgtgc	agaccgcag	cgcagaggag												180
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				Met Ala Glu Leu Asn Thr His													
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Val Asn Val Lys Glu Lys Ile Tyr Ala Val Arg Ser Val Val Pro Asn																	
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Lys Ser Asn Asn Glu Ile Val Leu Val Leu Gln Gln Phe Asp Phe Asn																	
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gtg gat aaa gcc gtg caa gcc ttt gtg gat ggc agt gca att caa gtt																	496
Val Asp Lys Ala Val Gln Ala Phe Val Asp Gly Ser Ala Ile Gln Val																	
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Leu Lys Glu Trp Asn Met Thr Gly Lys Lys Lys Asn Asn Lys Arg Lys																	
				60					65						70		
aga agc aag tcc aag cag cat caa ggc aac aaa gat gct aaa gac aag																	592
Arg Ser Lys Ser Lys Gln His Gln Gly Asn Lys Asp Ala Lys Asp Lys																	
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Val Glu Arg Pro Glu Ala Gly Pro Leu Gln Pro Gln Pro Pro Gln Ile																	
	90						95					100					

caa Gln	aac Asn	ggc Gly	ccc Pro	atg Met	aat Asn	ggc Gly	tgc Cys	gag Glu	aaag Lys	gac Asp	agc Ser	tcg Ser	tcc Ser	aca Thr	gat Asp	688
105110115																
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ata Ile	ctt Leu	gag Glu	gaa Glu	cct Pro	tca Ser	aag Lys	gca Ala	ctt Leu	cgt Arg	ggg Gly	gtc Val	aca Thr	ggc Gly	cca Pro	aat Asn	784
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act Thr	ccc Pro	tgc Cys	agc Ser	tcc Ser	ctg Leu	ctg Leu	cct Pro	ctg Leu	ctg Leu	aat Asn	gcg Ala	cac His	gca Ala	gca Ala	acc Thr	1264
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2311

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ctttatgcag	actaaciaag	ggatcattct	gctgtgtacc	tgtccctatt	ctagaccctg	240
gtgggcagca	gtgggaccat	tctgaccaca	atgcctgta	atg atg ggg caa gag		294
				Met Met Gly Gln Glu		
				1 5		
aaa gtg ccc att aag cag gta cct ggg gga gtc aag cag ctt gag ccc						342
Lys Val Pro Ile Lys Gln Val Pro Gly Gly Val Lys Gln Leu Glu Pro						
	10		15		20	
ccc aaa gaa gga gaa agg cgg aca acc cat aat atc att gag aaa cga						390
Pro Lys Glu Gly Glu Arg Arg Thr Thr His Asn Ile Ile Glu Lys Arg						
	25		30		35	
tat cgc tcc tcc atc aat gac aaa atc atc gaa ttg aaa gac ctg gtc						438
Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu Leu Lys Asp Leu Val						
	40		45		50	
atg ggg aca gac gcc aag atg cac aag tct ggc gtt ctg agg aag gcc						486
Met Gly Thr Asp Ala Lys Met His Lys Ser Gly Val Leu Arg Lys Ala						
	55		60		65	
att gat tac acc aga tgc ctg aaa ggc ctc cat ggc ttt cct gcc ctt						534
Ile Asp Tyr Thr Arg Cys Leu Lys Gly Leu His Gly Phe Pro Ala Leu						
	70		75		80	85
cct ggt tcc gga cag ctg ggg aaa ggc cac agc agc tcc tct gct gcc						582
Pro Gly Ser Gly Gln Leu Gly Lys Gly His Ser Ser Ser Ser Ala Ala						
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ctg cag tct ttg ggg gcg ggg agg gct gga cat gtg gaa ccc tga tgc						630
Leu Gln Ser Leu Gly Ala Gly Arg Ala Gly His Val Glu Pro *						
	105		110		115	
agccgcagcg tcaaggacga ggaaggggtg ggaagggatg gtacgtggag gggaatgggt						690

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746

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Met Val Phe Leu Gln Asn His Val Arg Phe Phe Leu
1 5 10
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Glu Ser Leu Pro Ala Phe Leu Arg Val Leu Ile Gln Ala Gly Ala Leu
15 20 25
tgt tgg agt ctt cca gag ctc tcc caa gga gag gta ggg aag gga gct 504
Cys Trp Ser Leu Pro Glu Leu Ser Gln Gly Glu Val Gly Lys Gly Ala
30 35 40
tgt cca gca gaa gtt ggg aag cac aga gat cat ctg cct tct tct gac 552
Cys Pro Ala Glu Val Gly Lys His Arg Asp His Leu Pro Ser Ser Asp
45 50 55 60
ccg gta ttg atg cag gct gag gcc tct gtt gta atg tgc tgg gtg tca 600
Pro Val Leu Met Gln Ala Glu Ala Ser Val Val Met Cys Trp Val Ser
65 70 75
tct gaa gac aga agt gcc ctg tgg gct ttg gtt acg ttc tat ggg gga 648
Ser Glu Asp Arg Ser Ala Leu Trp Ala Leu Val Thr Phe Tyr Gly Gly
80 85 90

gat tgc cag cta acc ctc aat aag aaa tgc acg cat ttg att gtt cca	696
Asp Cys Gln Leu Thr Leu Asn Lys Lys Cys Thr His Leu Ile Val Pro	
95 100 105	
gag cca aag ggg ggg aaa tac gaa tgt gct tta aag cga gca agt att	744
Glu Pro Lys Gly Gly Lys Tyr Glu Cys Ala Leu Lys Arg Ala Ser Ile	
110 115 120	
aaa att gtg act cct gac tgg gtt ctg gat tgc gta tca gag aaa acc	792
Lys Ile Val Thr Pro Asp Trp Val Leu Asp Cys Val Ser Glu Lys Thr	
125 130 135 140	
aaa aag gac gaa gca ttt tat cat cct cgt ctg att att tat gaa gag	840
Lys Lys Asp Glu Ala Phe Tyr His Pro Arg Leu Ile Ile Tyr Glu Glu	
145 150 155	
gaa gaa gag gaa gag gaa gag gag gag gaa gta gaa aat gag gaa caa	888
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Val Glu Asn Glu Glu Gln	
160 165 170	
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Asp Ser Gln Asn Glu Gly Ser Thr Asp Glu Lys Ser Ser Pro Ala Ser	
175 180 185	
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Ser Gln Glu Gly Ser Pro Ser Gly Asp Gln Gln Phe Ser Pro Lys Ser	
190 195 200	
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Asn Thr Glu Lys Ser Lys Gly Glu Leu Met Phe Asp Asp Ser Ser Asp	
205 210 215 220	
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Ser Ser Pro Glu Lys Gln Glu Arg Asn Leu Asn Trp Thr Pro Ala Glu	
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Val Pro Gln Leu Ala Ala Ala Lys Arg Arg Leu Pro Gln Gly Lys Glu	
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cct ggg ttg att aac ttg tgt gcc aat gtc cca ccc gtc cca ggt aac	1176
Pro Gly Leu Ile Asn Leu Cys Ala Asn Val Pro Pro Val Pro Gly Asn	
255 260 265	
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Ile Leu Pro Pro Glu Val Arg Gly Asn Leu Met Ala Ala Gly Gln Asn	
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Leu Gln Ser Ser Glu Arg Ser Glu Met Ile Ala Thr Trp Ser Pro Ala	
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Val Arg Thr Leu Arg Asn Ile Thr Asn Asn Ala Asp Ile Gln Gln Met	
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Ala	Gly	Ala	Lys	Tyr	Thr	Gly	Tyr	Leu	Cys	Arg	Ser	Asn	Thr	Val	Leu			
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Ile	Cys	Lys	Glu	Pro	Thr	Gly	Leu	Lys	Tyr	Glu	Lys	Ala	Lys	Glu	Trp			
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Asn	Phe	Glu	Ala	Leu	Arg	Gln	Ile	Gln	Tyr	Ser	Arg	Tyr	Thr	Ala	Phe			
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agt	ctg	cag	gat	cca	ttt	gcc	cct	acc	cag	cat	tta	gtt	tta	aat	ctt		2328	
Ser	Leu	Gln	Asp	Pro	Phe	Ala	Pro	Thr	Gln	His	Leu	Val	Leu	Asn	Leu			
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Leu	Asp	Ala	Trp	Arg	Val	Pro	Leu	Lys	Val	Ser	Ala	Glu	Leu	Leu	Met			
655				660				665										
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Ser	Ile	Arg	Leu	Pro	Pro	Lys	Leu	Lys	Gln	Asn	Glu	Val	Ala	Asn	Val			
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Gln	Pro	Ser	Ser	Gln	Arg	Ala	Arg	Ile	Glu	Asp	Val	Pro	Pro	Pro	Thr			
685				690				695										
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Lys	Lys	Leu	Thr	Pro	Glu	Leu	Thr	Pro	Phe	Val	Leu	Phe	Thr	Gly	Phe			
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Glu	Pro	Val	Gln	Val	Gln	Gln	Tyr	Ile	Lys	Lys	Leu	Tyr	Ile	Leu	Gly			
720				725				730										
gga	gag	gtt	gcg	gag	tct	gca	cag	aag	tgc	aca	cac	ctc	att	gcc	agc		2616	
Gly	Glu	Val	Ala	Glu	Ser	Ala	Gln	Lys	Cys	Thr	His	Leu	Ile	Ala	Ser			
735				740				745										
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Lys	Val	Thr	Arg	Thr	Val	Lys	Phe	Leu	Thr	Ala	Ile	Ser	Val	Val	Lys			
750				755				760										
cac	ata	gtg	acg	cca	gag	tgg	ctg	gaa	gaa	tgc	ttc	agg	tgt	cag	aag		2712	
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Leu Pro Pro Cys Ser Leu Ile Ser Asp Cys Cys Ala Ser Asn Gln Arg
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Asp Ser Val Gly Val Gly Pro Ser Glu Pro Gly Val Gly Tyr Ser Leu
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Val Val Arg Arg Phe Leu Ser Arg Ser Glu Lys Arg Asn Ile Arg Val
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Gly Val Thr Arg Phe Ser Arg Cys Val Arg His Pro Phe Leu *
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                                   Met Ser Gly Arg
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Ser Gly Tyr Arg Leu Ser Leu Leu Leu Leu Ala Ala Leu Gly Ser Gly
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cgc gcg gag cgc gac tgc cga gtg agc agc ttc cga gtc aag gag aac      329
Arg Ala Glu Arg Asp Cys Arg Val Ser Ser Phe Arg Val Lys Glu Asn
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ttc gac aag gct cgc ttc tct ggg acc tgg tac gcc atg gcc aag aag      377
Phe Asp Lys Ala Arg Phe Ser Gly Thr Trp Tyr Ala Met Ala Lys Lys
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gac ccc gag ggc ctc ttt ctg cag gac aac atc gtc gcg gag ttc tcc      425
Asp Pro Glu Gly Leu Phe Leu Gln Asp Asn Ile Val Ala Glu Phe Ser
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gtg gac gag acc ggc cag atg agc gcc aca gcc aag ggc cga gtc cgt      473
Val Asp Glu Thr Gly Gln Met Ser Ala Thr Ala Lys Gly Arg Val Arg
                70                               75                               80

ctt ttg aat aac tgg gac gtg tgc gca gac atg gtg ggc acc ttc aca      521
Leu Leu Asn Asn Trp Asp Val Cys Ala Asp Met Val Gly Thr Phe Thr
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Asp Thr Glu Asp Pro Ala Lys Phe Lys Met Lys Tyr Trp Gly Val Ala
                105                               110                               115

tcc ttt ctc cag aaa gga aat gat gac cac tgg atc gtc gac aca gac      617
Ser Phe Leu Gln Lys Gly Asn Asp Asp His Trp Ile Val Asp Thr Asp
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tac gac acg tat gcc gtg cag tac tcc tgc cgc ctc ctg aac ctc gat      665
Tyr Asp Thr Tyr Ala Val Gln Tyr Ser Cys Arg Leu Leu Asn Leu Asp
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Gly Leu Pro Pro Glu Ala Gln Lys Ile Val Arg Gln Arg Gln Glu Glu	
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Leu Cys Leu Ala Arg Gln Tyr Arg Leu Ile Val His Asn Gly Tyr Cys	
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Asp Gly Arg Ser Glu Arg Asn Leu Leu *	
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Asp Ser Ser Ser Leu Ala Leu Pro Ser Glu Ala Lys Leu Lys Leu Ala	
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Gly Ser Ser Gly Arg Gly Gly Gln Thr Val Lys Ser Leu Arg Ile Gln	
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Leu Ile Asp Ser Leu Val His Tyr Val Arg Gly Thr Ile Ala Asp Tyr	
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Gln Pro Asp Asp Lys Ala Thr Glu Asn Cys Val Cys Ile Leu His Asn	
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Trp His Ser Ile Val Ile Arg Met Tyr Leu Ser Leu Ile Ala Lys Ser	
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Thr Ala Gly Ser Gly Pro Met Pro Thr Ser Val Ala Gln Thr Val Val	
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Gln Lys Glu Ser Gly Leu Gln His Thr Arg Lys Met Leu His Val Gly	
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Asp Pro Ser Val Lys Lys Thr Ala Ile Ser Leu Leu Arg Asn Leu Ser	
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cgg aat ctt tct ctg cag aat gaa att gcc aaa gaa act ctc cct gat	2212
Arg Asn Leu Ser Leu Gln Asn Glu Ile Ala Lys Glu Thr Leu Pro Asp	
715 720 725	
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Leu Tyr Gly Asp Leu Gln Arg Phe Gly Arg Arg Ile Asp Leu Arg Val
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Lys Thr Gly Ala Glu Ala Ile Arg Ala Leu Ala Thr Gln Leu Pro Ala
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Arg Asp Val Ser Thr Ser Gly Leu Thr Ala Gln Leu His Glu Thr Leu	
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Pro Asp Gly Ala Val Ile His Ile Val Pro Arg Val Ala Gly Ala Lys	
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Ser Gly Gly Val Phe Gln Ile Val Leu Gly Ala Ala Ala Ile Ala Gly	
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Ser Phe Phe Thr Ala Gly Ala Thr Leu Ala Ala Trp Gly Ala Ala Ile	
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Gly Ala Gly Gly Met Thr Gly Ile Leu Phe Ser Leu Gly Ala Ser Met	
135 140 145	
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Val Leu Gly Gly Val Ala Gln Met Leu Ala Pro Lys Ala Arg Thr Pro	
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Arg Ile Gln Thr Thr Asp Asn Gly Lys Gln Asn Thr Tyr Phe Ser Ser	
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Leu Asp Asn Met Val Ala Gln Gly Asn Val Leu Pro Val Leu Tyr Gly	
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Glu Met Arg Val Gly Ser Arg Val Val Ser Gln Glu Ile Ser Thr Ala	
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 Met Asp Asp Leu Thr
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 Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln Arg Ser Arg Lys
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 Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln Trp Pro Glu Glu
 25 30 35
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 Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp Glu Gln Asn Ser
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 Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys Pro Leu Gly Gly
 55 60 65
 ggt aca cca aaa gaa gag cca aca atg aaa act tct aaa aaa gga agc 355
 Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser Lys Lys Gly Ser
 70 75 80 85
 aaa aaa aaa tct gga cct cca gca cca gag gag gag gaa gaa gaa gaa 403
 Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu Glu Glu Glu Glu
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 Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser Lys Gln His Arg
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 Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg Gly Arg Pro Ser
 135 140 145
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 Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val Arg Val Gly Arg

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ccc Pro	gcc Ala	gcc Ala 50	cac His	gtc Val	gca Ala	gga Gly	aac Asn 55	ccc Pro	ggt Gly	ggg Gly	gac Asp	gcg Ala 60	gcc Ala	ccc Pro	gca Ala	432
gcc Ala	acg Thr 65	ggc Gly	acc Thr	gcg Ala	gcc Ala	gcc Ala 70	gcc Ala	tct Ser	tta Leu	gcc Ala	acc Thr 75	gcc Ala	gcc Ala	ggc Gly	agc Ser	480
gaa Glu 80	gac Asp	gcg Ala	gag Glu	aaa Lys	aaa Lys 85	gtt Val	ctc Leu	gcc Ala	acc Thr	aaa Lys 90	gtc Val	ctt Leu	ggc Gly	act Thr	gtc Val 95	528
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acc Thr	aaa Lys	gaa Glu	gat Asp 115	gta Val	ttt Phe	gta Val	cat His	cag Gln 120	act Thr	gcc Ala	atc Ile	aag Lys	aag Lys 125	aat Asn	aac Asn	624
cca Pro	cgg Arg	aaa Lys 130	tat Tyr	ctg Leu	cgc Arg	agt Ser	gta Val 135	gga Gly	gat Asp	gga Gly	gaa Glu	act Thr 140	gta Val	gag Glu	ttt Phe	672
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Gly	Ala	Ala	Val	Cys	Ala	Tyr	Val	Arg	Met	Val	Phe	Leu	Ala	Leu	Tyr	
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Val	Leu	Phe	Leu	Ala	Asp	Glu	Glu	Phe	Asp	Val	Val	Val	Cys	Asp	Gln	
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Val	Ser	Ala	Cys	Ile	Pro	Val	Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	
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atc	cta	ttt	tac	tgt	cac	ttc	cca	gat	ctg	ctt	ctc	acc	aag	aga	gat	486
Ile	Leu	Phe	Tyr	Cys	His	Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	
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Ser	Phe	Leu	Lys	Arg	Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	
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Ala	Ala	Val	Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	
185					190					195						
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Asp	Val	Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	
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Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	Trp	Glu	
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Lys Pro Cys Gly Cys Arg Glu Cys Gly Lys Ala Phe Phe Gln Lys Ser	

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Arg Ala Ala Ala Ala Val Glu Pro Asp Val Val Val Lys Arg Gln Glu	
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Val Glu Lys His Lys Glu Lys Leu Lys Gln Leu Glu Glu Glu Lys Arg	
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Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Lys Ser Tyr	
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Lys Gly Asn Ala Lys Lys Pro Gln Glu Glu Asp Ser Pro Gly Pro Ser	
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 Phe Glu Pro Leu Arg Val Pro Pro Asp Leu Phe Arg Arg Leu Thr Gly
 135 140 145

cag ttt tgc atg atc caa acc ttg aaa aag ggc caa act tat gct gca 595
 Gln Phe Cys Met Ile Gln Thr Leu Lys Lys Gly Gln Thr Tyr Ala Ala
 150 155 160

gag Glu	gat Asp 165	aaa Lys	acc Thr	tca Ser	gtt Val	gat Asp 170	gac Asp	cgt Arg	ctg Leu	agt Ser	att Ile 175	ctc Leu	ttg Leu	aag Lys	gga Gly	643
aaa Lys 180	atg Met	aag Lys	gtc Val	tcc Ser	tat Tyr 185	cga Arg	gga Gly	cat His	ttt Phe	ctg Leu 190	cat His	aac Asn	att Ile	tac Tyr	ccc Pro 195	691
tgt Cys	gcc Ala	ttt Phe	ata Ile	gat Asp 200	tct Ser	cct Pro	gaa Glu	ttt Phe	aga Arg 205	tca Ser	act Thr	cag Gln	atg Met	cac His	aaa Lys 210	739
ggg Gly	gaa Glu	aaa Lys	ttc Phe 215	cag Gln	gtc Val	acc Thr	att Ile 220	att Ile	gca Ala	gat Asp	gat Asp	aac Asn	tgc Cys 225	aga Arg	ttt Phe	787
tta Leu	tgc Cys	tgg Trp 230	tca Ser	aga Arg	gaa Glu	aga Arg	tta Leu 235	aca Thr	tac Tyr	ttt Phe	ctg Leu 240	gaa Glu	tca Ser	gaa Glu	cct Pro	835
ttc Phe 245	ttg Leu	tat Tyr	gaa Glu	atc Ile	ttt Phe	agg Arg 250	tat Tyr	ctt Leu	att Ile	gga Gly 255	aaa Lys 255	gac Asp	atc Ile	aca Thr	aat Asn	883
aag Lys 260	ctc Leu	tac Tyr	tca Ser	ttg Leu	aat Asn 265	gat Asp	ccc Pro	acc Thr	tta Leu	aat Asn 270	gat Asp	aaa Lys	aaa Lys	gcc Ala	aaa Lys 275	931
aag Lys	ctg Leu	gaa Glu	cat His	cag Gln 280	ctc Leu	agc Ser	ctc Leu	tgc Cys	aca Thr 285	cag Gln	atc Ile	tcc Ser	atg Met	ttg Leu 290	gaa Glu	979
atg Met	agg Arg	aac Asn	agt Ser 295	ata Ile	gcc Ala	agc Ser	tcc Ser	agt Ser 300	gac Asp	agt Ser	gac Asp	gac Asp	ggc Gly 305	ttg Leu	cac His	1027
cag Gln	ttt Phe 310	ctt Leu	cgg Arg	ggg Gly	acc Thr	tcc Ser	agc Ser 315	atg Met	tcc Ser	tct Ser	ctt Leu 320	cat His	gtg Val	tca Ser	tcc Ser	1075
cca Pro	cac His 325	cag Gln	cga Arg	gcc Ala	tct Ser	gcc Ala 330	aag Lys	atg Met	aaa Lys	ccg Pro 335	ata Ile	gaa Glu	gaa Glu	gga Gly	gca Ala	1123
gaa Glu 340	gat Asp	gat Asp	gat Asp	gac Asp	gtt Val 345	ttt Phe	gaa Glu	ccg Pro	gca Ala	tct Ser 350	cca Pro	aat Asn	aca Thr	ttg Leu	aaa Lys 355	1171
gtc Val	cat His	cag Gln	ctg Leu	cct Pro	tga *	tcagag	agagaattca	ggttaccaag	acggaaggtg	1225						
tcttgaagag	atcctgaaaa	ataccagcac	tttttcatgg	cttttagggt	attctgcttt	1285										
agtgcattcca	gactggtaga	gtcggaggga	ggaagtgagg	aaggggtcaag	gatggaagag	1345										
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aaaaaaa

1412

<210> 27
<211> 1861
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (325) .. (1242)

<400> 27

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agactgttcg ccccgccctg agtactccta tcttgtttct ccacctgttc gggagttgga	180
gatgtgcacc taaaggaggc gcatctgggg acggacacat ctggcactga ggccctcgcc	240
acctgcctcg ccacctggcg acctgaccc caccacactg ccttgagagt cgctcaaaag	300
tagggcccca gggctcgcag cagc atg ggc acc gag aaa gaa agc cca gag	351
Met Gly Thr Glu Lys Glu Ser Pro Glu	
1 5	
ccc gac tgc cag aaa cag ttc cag gct gca gtg agc gtc atc cag aac	399
Pro Asp Cys Gln Lys Gln Phe Gln Ala Ala Val Ser Val Ile Gln Asn	
10 15 20 25	
ctg ccc aag aac ggt tct tac cgc ccc tcc tat gaa gag atg ctg cga	447
Leu Pro Lys Asn Gly Ser Tyr Arg Pro Ser Tyr Glu Glu Met Leu Arg	
30 35 40	
ttc tac agt tac tac aag cag gcc acc atg ggg ccc tgc ctg gtc ccc	495
Phe Tyr Ser Tyr Tyr Lys Gln Ala Thr Met Gly Pro Cys Leu Val Pro	
45 50 55	
cgg ccc ggg ttc tgg gac ccc att gga cga tat aag tgg gac gcc tgg	543
Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr Lys Trp Asp Ala Trp	
60 65 70	
aac agt ctg ggc aag atg agc agg gag gag gcc atg tct gcc tac atc	591
Asn Ser Leu Gly Lys Met Ser Arg Glu Glu Ala Met Ser Ala Tyr Ile	
75 80 85	
act gaa atg aaa ctg gtg gca cag aag gtg atc gac aca gtg ccc ctg	639
Thr Glu Met Lys Leu Val Ala Gln Lys Val Ile Asp Thr Val Pro Leu	
90 95 100 105	
ggg gag gtg gca gag gac atg ttt ggt tac ttc gag ccc ctg tac cag	687
Gly Glu Val Ala Glu Asp Met Phe Gly Tyr Phe Glu Pro Leu Tyr Gln	
110 115 120	

gtg atc cct gac atg ccg agg ccc cca gag acc ttc ctg aga agg gtc Val Ile Pro Asp Met Pro Arg Pro Pro Glu Thr Phe Leu Arg Arg Val 125 130 135	735
aca ggt tgg aaa gag cag gtt gtg aat gga gat gtt ggg gct gtt tca Thr Gly Trp Lys Glu Gln Val Val Asn Gly Asp Val Gly Ala Val Ser 140 145 150	783
gag cct ccc tgc ctc ccc aag gaa ccg gca ccc cca agc cca gag tcc Glu Pro Pro Cys Leu Pro Lys Glu Pro Ala Pro Pro Ser Pro Glu Ser 155 160 165	831
cat tca ccc agg gac ctg gac tcc gag gtt ttc tgt gat tcc ctg gag His Ser Pro Arg Asp Leu Asp Ser Glu Val Phe Cys Asp Ser Leu Glu 170 175 180 185	879
cag ctg gag cct gag ctg gtt tgg aca gag cag cgg gca gca tct gga Gln Leu Glu Pro Glu Leu Val Trp Thr Glu Gln Arg Ala Ala Ser Gly 190 195 200	927
gga aag cgt gat ccc agg aac agc ccc gtg ccc ccc aca aag aaa gag Gly Lys Arg Asp Pro Arg Asn Ser Pro Val Pro Pro Thr Lys Lys Glu 205 210 215	975
ggg ttg cgg ggc agc ccg ccg ggg ccc cag gag ttg gac gtg tgg ctg Gly Leu Arg Gly Ser Pro Pro Gly Pro Gln Glu Leu Asp Val Trp Leu 220 225 230	1023
ctg ggg aca gtt cga gca cta cag gag agc atg cag gag gtg cag gcg Leu Gly Thr Val Arg Ala Leu Gln Glu Ser Met Gln Glu Val Gln Ala 235 240 245	1071
agg gtg cag agc ctg gag agc atg ccc cgg ccc cct gag cag agg ccg Arg Val Gln Ser Leu Glu Ser Met Pro Arg Pro Pro Glu Gln Arg Pro 250 255 260 265	1119
cag ccc agg ccc agt gct cgg cca tgg ccc ctt ggg ctc ccg ggg ccc Gln Pro Arg Pro Ser Ala Arg Pro Trp Pro Leu Gly Leu Pro Gly Pro 270 275 280	1167
gcg ctg ctc ttc ttc ctc ctg tgg ccc ttc gtc gtc cag tgg ctc ttc Ala Leu Leu Phe Phe Leu Leu Trp Pro Phe Val Val Gln Trp Leu Phe 285 290 295	1215
cga atg ttt cgg acc caa aag agg tga ctgtc agtggagggg tctctgcagc Arg Met Phe Arg Thr Gln Lys Arg *	1267
300 305	
caactgagac tatcttgctg tgccctgagc cttcctaggg tttagaagaa cagcattcaa	1327
aattccccgt cctgtcagtg ttgacctcg cacctcctcc cctaaagcag cgcggggggc	1387
aaataagacc ccaccctcc ctgcagcttc acaggagcgc ttccttccct ccccgcaacc	1447
acccagggct cccctgggag gctgcagttg tggtacacgt ccccggtgct gggttggccg	1507

tgactcgggg gcggggcat cgggtctcag cccctgcctt cccagtcctc tgggtcaccc 1567
gaattttccc acccctgctt ctccccgagg aggttgagct cttgagcaag ttgggacttg 1627
ggccgggggcc tggaagaatg attggctggg agggcgcggg agggaggcca ggaggcccg 1687
accagttggg aggagtgagc agggcccggg ggagggggat gagcgagtt tgctcgcttt 1747
cctccccctgc cggccccctc cgccccaca cacactcggg acgtcttcat tgaagattca 1807
cttacaaagg aatgtttcac taaataaaag aaaaccagaa aaaaaaaaaa aaaa 1861

<210> 28
<211> 997
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (151)..(912)

<400> 28
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ggaccaccct gcggggcgca ccagcgatct ggggtgcggg gctcggcctc cctgcgctcc 120
tggctgacgg tgtgaccttg ggtcttaacc atg aac ttc tct gga gga ggg 171
Met Asn Phe Ser Gly Gly Gly
1 5
agg cag gaa gca gca ggg tcc agg ggt aga agg gct ccc aga ccc cga 219
Arg Gln Glu Ala Ala Gly Ser Arg Gly Arg Arg Ala Pro Arg Pro Arg
10 15 20
gaa cag gac cga gac gtg cag ctg tcc aag gct ctg tcc tat gcc ctg 267
Glu Gln Asp Arg Asp Val Gln Leu Ser Lys Ala Leu Ser Tyr Ala Leu
25 30 35
cgc cat ggg gcc ttg aag ctg ggg ctt ccc atg gga gct gat ggc ttc 315
Arg His Gly Ala Leu Lys Leu Gly Leu Pro Met Gly Ala Asp Gly Phe
40 45 50 55
gtg ccc ctg ggc acc ctg ctg cag ttg ccc cag ttc cgc ggc ttc tct 363
Val Pro Leu Gly Thr Leu Leu Gln Leu Pro Gln Phe Arg Gly Phe Ser
60 65 70
gct gaa gat gtg cag cgc gtg gtg gac acc aat agg aag cag cgg ttc 411
Ala Glu Asp Val Gln Arg Val Val Asp Thr Asn Arg Lys Gln Arg Phe
75 80 85
gcc ctg cag ctg ggg gat ccc agc act ggc ctt ctg atc cgg gcc aac 459
Ala Leu Gln Leu Gly Asp Pro Ser Thr Gly Leu Leu Ile Arg Ala Asn
90 95 100

006T60T49660

cag ggc cat tcc ctg cag gta cct aag ttg gag ctg atg ccc ctg gag Gln Gly His Ser Leu Gln Val Pro Lys Leu Glu Leu Met Pro Leu Glu 105 110 115	507
aca ccg cag gcc ctg ccc ccg atg cta gtc cat ggt aca ttc tgg aag Thr Pro Gln Ala Leu Pro Pro Met Leu Val His Gly Thr Phe Trp Lys 120 125 130 135	555
cac tgg cca tcc atc cta ctc aaa ggc ctg tcc tgc cag gga agg acg His Trp Pro Ser Ile Leu Leu Lys Gly Leu Ser Cys Gln Gly Arg Thr 140 145 150	603
cac att cac ctg gcc cca gga ctg cct gga gac ccc ggt atc atc agt His Ile His Leu Ala Pro Gly Leu Pro Gly Asp Pro Gly Ile Ile Ser 155 160 165	651
ggc atg cgg tcc cat tgt gaa ata gct gtg ttc atc gat gga ccc ctg Gly Met Arg Ser His Cys Glu Ile Ala Val Phe Ile Asp Gly Pro Leu 170 175 180	699
gct ctg gca gat gga ata ccc ttc ttc cgc tct gcc aat ggg gtg att Ala Leu Ala Asp Gly Ile Pro Phe Phe Arg Ser Ala Asn Gly Val Ile 185 190 195	747
ctg act cca ggg aat act gat ggc ttc ctc ctt ccc aag tac ttc aag Leu Thr Pro Gly Asn Thr Asp Gly Phe Leu Leu Pro Lys Tyr Phe Lys 200 205 210 215	795
gag gcc ctg cag cta cgc cct acc cga aag ccc ctt tcc ttg gct ggt Glu Ala Leu Gln Leu Arg Pro Thr Arg Lys Pro Leu Ser Leu Ala Gly 220 225 230	843
gat gaa gag aca gag tgt cag agt agc ccc aag cac agc tcc aga gaa Asp Glu Glu Thr Glu Cys Gln Ser Ser Pro Lys His Ser Ser Arg Glu 235 240 245	891
agg agg agg atc caa caa taa aa tattaattta taaaaaagaa attttaaaaa Arg Arg Arg Ile Gln Gln *	944
250	
gtaacaagaa agaactcgtt tgaaaccatg tttcatcaaa aaaaaaaaaa aaa	997

<210> 29
<211> 1138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (232) .. (1026)

<400> 29
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000409 143450

cccacgcgtc cggctgagaa ggctacatgt gacgagaatg attctgtttc aaatatagcc	120
acagaaataa aggagggaca acaatctggg acagtgtctc ctcagaaaca atcggcccag	180
aaggttatat ttaaaaagaa agtttctctt ttgaatattg ccacaagaat a atg ggc	237
	Met Gly
	1
ggt ggg aaa tct gga aca gtg tct tct cag aaa caa cca gcc tca aag	285
Gly Gly Lys Ser Gly Thr Val Ser Ser Gln Lys Gln Pro Ala Ser Lys	
5 10 15	
act gca agt gac aag aca gat tct gct ttg aat aca gct aca gaa ata	333
Thr Ala Ser Asp Lys Thr Asp Ser Ala Leu Asn Thr Ala Thr Glu Ile	
20 25 30	
aag gat gga cta caa tgt ggg aca gtg tct tct cag aaa caa caa gcc	381
Lys Asp Gly Leu Gln Cys Gly Thr Val Ser Ser Gln Lys Gln Gln Ala	
35 40 45 50	
ttg aag gct aca act gac gag gaa ggt tct gtt tct aat ata gcc aca	429
Leu Lys Ala Thr Thr Asp Glu Glu Gly Ser Val Ser Asn Ile Ala Thr	
55 60 65	
gaa ata aag gat gga gaa aaa tct ggg aca gtg tct tct cag aaa aaa	477
Glu Ile Lys Asp Gly Glu Lys Ser Gly Thr Val Ser Ser Gln Lys Lys	
70 75 80	
cca gcc ttg aag gcc aca agt gat gag aaa gat tct ttt tcg aat ata	525
Pro Ala Leu Lys Ala Thr Ser Asp Glu Lys Asp Ser Phe Ser Asn Ile	
85 90 95	
acc aga gaa aaa aag gat gga gaa ata tct agg aca gtg tct tct cag	573
Thr Arg Glu Lys Lys Asp Gly Glu Ile Ser Arg Thr Val Ser Ser Gln	
100 105 110	
aaa cca cca gcc ttg aag gct aca agt gtc aag gaa gat tct gtt ttg	621
Lys Pro Pro Ala Leu Lys Ala Thr Ser Val Lys Glu Asp Ser Val Leu	
115 120 125 130	
aat ata gcc aga gaa aaa aag gat gga gaa aaa tct agg aca gtg tct	669
Asn Ile Ala Arg Glu Lys Lys Asp Gly Glu Lys Ser Arg Thr Val Ser	
135 140 145	
ttt gac caa cca cca ggc ttg aag gct aca aga gac gag aaa gat tct	717
Phe Asp Gln Pro Pro Gly Leu Lys Ala Thr Arg Asp Glu Lys Asp Ser	
150 155 160	
ctt ttg aat ata gcc aga gga aaa gag gat gga gaa aaa act agg aga	765
Leu Leu Asn Ile Ala Arg Gly Lys Glu Asp Gly Glu Lys Thr Arg Arg	
165 170 175	
gtg tct tct cgg aaa aaa cca gcc ttg aag gct aca agt gat gag aaa	813
Val Ser Ser Arg Lys Lys Pro Ala Leu Lys Ala Thr Ser Asp Glu Lys	
180 185 190	
gat tct ttt tcg aat ata acc aga gaa aaa aag gat gga gaa aca tct	861

Asp Ser Phe Ser Asn Ile Thr Arg Glu Lys Lys Asp Gly Glu Thr Ser
195 200 205 210

agg aca gtg tct tct cag aaa cca cca gcc ttg aag gct aca agt gac 909
Arg Thr Val Ser Ser Gln Lys Pro Pro Ala Leu Lys Ala Thr Ser Asp
215 220 225

gag gaa gat tct gtt ttg agt ata gcc aga gaa gaa aag gat gga gaa 957
Glu Glu Asp Ser Val Leu Ser Ile Ala Arg Glu Glu Lys Asp Gly Glu
230 235 240

aaa tct agg aca gtg tct tct gag caa cca cca ggc ttg aag tgt ctt 1005
Lys Ser Arg Thr Val Ser Ser Glu Gln Pro Pro Gly Leu Lys Cys Leu
245 250 255

ctc gga aaa aag cag cct tga ag gctacaagtg atgagaaaga ttctttttca 1058
Leu Gly Lys Lys Gln Pro *
260 265

aatataacca gagaaagaaa ggaaggagaa acatctagga cagtgtcttc tcagaaacca 1118

ccagccttga aggctacaag 1138

<210> 30
<211> 1270
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (274)..(1173)

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ccgcgggagc caggaggagc caactgcgcc ggaggagggg ttccggccga cagtcgggga 180

ttggcggctg cagccagggg tcttcgcagc ctgggcttcc gtgagcggcg ctctgccaga 240

tctctggacc ggattcgtcc cattctcgtc ctc atg gtg gac aag aaa ctg gtg 294
Met Val Asp Lys Lys Leu Val
1 5

gtg gtt ttc gga ggc aca ggt gcc cag ggt ggc tcc gtg gcc cgc aca 342
Val Val Phe Gly Gly Thr Gly Ala Gln Gly Gly Ser Val Ala Arg Thr
10 15 20

ctc ctg gaa gat ggg aca ttc aag gtt cga gtg gtg acc cga aac cct 390
Leu Leu Glu Asp Gly Thr Phe Lys Val Arg Val Val Thr Arg Asn Pro
25 30 35

agg aag aag gca gca aag gag ctg agg ctg caa ggt gca gaa gta gtg 438

00544.001900

Arg 40	Lys	Lys	Ala	Ala	Lys 45	Glu	Leu	Arg	Leu	Gln 50	Gly	Ala	Glu	Val 55		
cag Gln	gga Gly	gac Asp	caa Gln	gat Asp 60	gac Asp	cag Gln	gtc Val	atc Ile	atg Met 65	gag Glu	ctg Leu	gcc Ala	ctg Leu	aat Asn 70	ggg Gly	486
gct Ala	tac Tyr	gcc Ala	acc Thr 75	ttc Phe	atc Ile	gtg Val	acc Thr	aat Asn 80	tac Tyr	tgg Trp	gag Glu	agc Ser	tgc Cys 85	agc Ser	cag Gln	534
gag Glu	cag Gln	gag Glu 90	gtc Val	aag Lys	cag Gln	ggg Gly 95	aag Lys	ctg Leu	ctc Leu	gct Ala	gat Asp 100	ctg Leu	gcc Ala	agg Arg	cgc Arg	582
ctg Leu 105	ggc Gly	ctc Leu	cac His	tat Tyr	gtg Val	gtc Val 110	tac Tyr	agc Ser	ggc Gly	ctg Leu 115	gag Glu	aac Asn	atc Ile	aag Lys	aag Lys	630
ctg Leu 120	acg Thr	gca Ala	ggg Gly	aga Arg	ttg Leu 125	gcc Ala	gcc Ala	gcg Ala	cac His	ttt Phe 130	gac Asp	ggc Gly	aaa Lys	ggg Gly	gag Glu 135	678
gtg Val	gag Glu	gaa Glu	tat Tyr 140	ttc Phe	cgg Arg	gac Asp	att Ile	ggc Gly	gtt Val 145	ccc Pro	atg Met	acc Thr	agt Ser	gtg Val 150	cgg Arg	726
ctg Leu	ccc Pro	tgc Cys	tat Tyr 155	ttt Phe	gag Glu	aac Asn	ctc Leu	ctc Leu	tcc Ser	cac His	ttc Phe	ttg Leu	ccc Pro	cag Gln 165	aaa Lys	774
gcc Ala	cca Pro	gac Asp 170	gga Gly	aag Lys	agc Ser	tac Tyr	ttg Leu 175	ctg Leu	agc Ser	ttg Leu	ccc Pro	aca Thr 180	ggt Gly	gac Asp	gtt Val	822
ccc Pro 185	atg Met	gat Asp	ggc Gly	atg Met	tcc Ser	gtg Val 190	tct Ser	gac Asp	ctg Leu	ggt Gly	cct Pro	gtg Val	gtg Val	ctc Leu	agc Ser	870
ctt Leu 200	ttg Leu	aag Lys	atg Met	cca Pro	gaa Glu 205	aaa Lys	tac Tyr	gtc Val	ggc Gly 210	cag Gln	aac Asn	atc Ile	ggg Gly	ctg Leu 215	agc Ser	918
act Thr	tgc Cys	agg Arg	cac His 220	acg Thr	gcc Ala	gag Glu	gag Glu	tac Tyr	gct Ala 225	gcc Ala	ctg Leu	ctc Leu	acc Thr	aag Lys 230	cac His	966
acc Thr	cgc Arg	aag Lys	gtc Val 235	gtg Val	cac His	gat Asp	gcc Ala	aag Lys 240	atg Met	act Thr	cct Pro	gag Glu	gac Asp 245	tac Tyr	gaa Glu	1014
aag Lys	ctt Leu	ggc Gly 250	ttt Phe	ccc Pro	ggt Gly	gcc Ala	cgg Arg 255	gac Asp	ctg Leu	gcc Ala	aac Asn	atg Met 260	ttc Phe	cgt Arg	ttc Phe	1062
tat Tyr	gcc Ala	ctg Leu	aga Arg	ccc Pro	gac Asp	cgt Arg	gac Asp	atc Ile	gag Glu	ctg Leu	acc Thr	ctg Leu	aga Arg	ctc Leu	aac Asn	1110

265	270	275	
ccc aag gcc ctg acg ctg gac cag tgg ctg gaa cag cac aaa ggg gac			1158
Pro Lys Ala Leu Thr Leu Asp Gln Trp Leu Glu Gln His Lys Gly Asp			
280	285	290	295
ttc aac ctg ctg tga cctgccccgcc tcgcggcccc ttgtggggat cgggggcacc			1213
Phe Asn Leu Leu *			
300			
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<210> 31
 <211> 3053
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (454) .. (2802)
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 <221> misc_feature
 <222> (1) ... (3053)
 <223> n = a,t,c or g

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aaaaaatggt ctttaaaact atgaagtggg taatgggatt aaagtattca aggaatgaga	120
tggaaatcct ggtaatgggt agaaacatag gtaaattctc ctttcccact taccaccaac	180
ctgtgtgaac aacaatcatt tctcattaat agtcaagaat gtgaagagat catgagtana	240
aagtcttgat cagaaattgt gtatagctgt gtccagcata aaaccttata taaaatgcat	300
atcatagaa gatgctcaag tatgtcatga aaaatatgaa gtttatttaa atatttatcc	360
aaattaaaga tttnctgtat tctctaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagcct	420
cgtgccgaat tcggcacgag ggctgtcgcc acc atg gct ccg cac cgc ccc gcg	474
Met Ala Pro His Arg Pro Ala	
1 5	
ccc gcg ctg ctt tgc gcg ctg tcc ctg gcg ctg tgc gcg ctg tcg ctg	522
Pro Ala Leu Leu Cys Ala Leu Ser Leu Ala Leu Cys Ala Leu Ser Leu	
10 15 20	
ccc gtc cgc gcg gcc act gcg tcg cgg ggg gcg tcc cag gcg ggg gcg	570
Pro Val Arg Ala Ala Thr Ala Ser Arg Gly Ala Ser Gln Ala Gly Ala	
25 30 35	
ccc cag ggg cgg gtg ccc gag gcg cgg ccc aac agc atg gtg gtg gaa	618

Pro Gln Gly Arg Val Pro Glu Ala Arg Pro Asn Ser Met Val Val Glu	
40 45 50 55	
cac ccc gag ttc ctc aag gca ggg aag gag cct ggc ctg cag atc tgg	666
His Pro Glu Phe Leu Lys Ala Gly Lys Glu Pro Gly Leu Gln Ile Trp	
60 65 70	
cgt gtg gag aag ttc gat ctg gtg ccc gtg ccc acc aac ctt tat gga	714
Arg Val Glu Lys Phe Asp Leu Val Pro Val Pro Thr Asn Leu Tyr Gly	
75 80 85	
gac ttc ttc acg ggc gac gcc tac gtc atc ctg aag aca gtg cag ctg	762
Asp Phe Phe Thr Gly Asp Ala Tyr Val Ile Leu Lys Thr Val Gln Leu	
90 95 100	
agg aac gga aat ctg cag tat gac ctc cac tac tgg ctg ggc aat gag	810
Arg Asn Gly Asn Leu Gln Tyr Asp Leu His Tyr Trp Leu Gly Asn Glu	
105 110 115	
tgc agc cag gat gag agc ggg gcg gcc gcc atc ttt acc gtg cag ctg	858
Cys Ser Gln Asp Glu Ser Gly Ala Ala Ala Ile Phe Thr Val Gln Leu	
120 125 130 135	
gat gac tac ctg aac ggc cgg gcc gtg cag cac cgt gag gtc cag ggc	906
Asp Asp Tyr Leu Asn Gly Arg Ala Val Gln His Arg Glu Val Gln Gly	
140 145 150	
ttc gag tcg gcc acc ttc cta ggc tac ttc aag tct ggc ctg aag tac	954
Phe Glu Ser Ala Thr Phe Leu Gly Tyr Phe Lys Ser Gly Leu Lys Tyr	
155 160 165	
aag aaa gga ggt gtg gca tca gga ttc aag cac gtg gta ccc aac gag	1002
Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val Val Pro Asn Glu	
170 175 180	
gtg gtg gtg cag aga ctc ttc cag gtc aaa ggg cgg cgt gtg gtc cgt	1050
Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg Arg Val Val Arg	
185 190 195	
gcc acc gag gta cct gtg tcc tgg gag agc ttc aac aat ggc gac tgc	1098
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B **Beckwith, J.** 1976. *The Ecology of the Great Lakes Basin*. New York: McGraw-Hill.

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L **Levings, C.D., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

M **Mann, H.B., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

N **Nelson, J.M., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

O **Odum, E.P., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

P **Parker, I.M., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

Q **Quinn, J.S., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

R **Rosen, B., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

S **Schindler, D.W., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

T **Tilman, D., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

V **Valentine, J.W., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

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X **Xie, P., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

Y **Yang, Z., and J.E. Cloern.** 1980. *Estuarine Ecology*. San Francisco: W.H. Freeman & Co.

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His	Gln	Asn	Gly	Ser	Met	Ala	Ala	Val	Asn	Gly	His	Thr	Asn	Ser	Phe				
				270				275				280							
tca	ccc	ctg	gaa	aac	aat	gtg	aag	cca	agg	aag	ctg	cgg	aag	gat	tga	1035			
Ser	Pro	Leu	Glu	Asn	Asn	Val	Lys	Pro	Arg	Lys	Leu	Arg	Lys	Asp	*				
285				290				295				300							
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